



Substitute 47113.txt

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Therion, Corporation
- (ii) TITLE OF THE INVENTION: Recombinant Pox Virus For
Immunization Against MUC1 Tumor-Associated Antigen
- (iii) NUMBER OF SEQUENCES: 21
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: NIXON PEABODY LLP
 - (B) STREET: 100 Summer Street
 - (C) CITY: Boston
 - (D) STATE: MA
 - (E) COUNTRY: USA
 - (F) ZIP: 02110-2131
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 10/057,136
 - (B) FILING DATE: 25-JAN-2002
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/366,670
 - (B) FILING DATE: 03-AUG-1999
 - (C) CLASSIFICATION:
- (viii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/US98/03693
 - (B) FILING DATE: 24-FEB-1998
 - (C) CLASSIFICATION:
- (ix) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 60/038,253
 - (B) FILING DATE: 24-FEB-1997
- (x) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Eisenstein, Ronald I
 - (B) REGISTRATION NUMBER: 30,628
 - (C) REFERENCE/DOCKET NUMBER: 700953-047113-C2-RCE
- (xi) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 617-345-6054
 - (B) TELEFAX: 617-345-1300
 - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
 1 5 10 15
 Arg Pro Ala Pro
 20

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGCTCCACCG CCCCCCAGC CCACGGTGTG ACCTCGGCC CGGACACCAG GCCGGCCCCG 60

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Pro Asp Thr Arg Pro Ala Pro
 1 5

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGCAGTACTG CACCACCGGC ACATGGCGTA ACATCAGCAC CTGATACAAG ACCTGCACCT 60

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGATCCACCG CGCCGCTGC GCACGGAGTG ACGTCGGCGC CCGACACGCG CCCCCTCCC 60

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGGTCAACAG CTCCTCCCGC TCATGGGGTT ACTTCTGCTC CAGATACTCG CCCAGCTCCA 60

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGTTCGACGG CCCCCCTGC TCACGGTGTA ACATCCGCCC CGGATACCAG ACCGGCCCCT 60

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGCAGACCG CACCGCCCGC ACACGGGGTC ACAAGCGCGC CAGACACTCG ACCTGCGCCA 60

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGAAGTACCG CTCCACCTGC ACACGGGGTC ACAAGCGCGC CAGACACTCG ACCTGCGCCA 60

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGGTCGACTG CCCCTCCGGC GCATGGTGTG ACCTCAGCTC CTGACACAAG GCCAGCCCCA 60

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGTTCAACGG CACCTCCAGC ACACGGAGTC ACGTCTGCAC CCGACACCCG TCCAGCTCCG 60

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGTAGTACAG CGCCACCCGC ACATGGCGTC ACGAGCGCTC CGGATACGAG ACCGGCGCCT 60

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGCTCCACCG CACCCCCAGC CCACGGTGTC ACCTCGGCCC CGGACACCAG GCGGGCCCCG 60
GGCTCCACCC CGGCCCCG 78

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGCTCCACCG CCCCCCAGC CCATGGTGTC ACCTCGGCCC CGGACAACAG GCCCGCCTTG 60

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGCTCCACCG CCCCTCCAGT CCACAATGTC ACCTCGGCC

39

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
 1 5 10 15
 Arg Arg Ala Pro
 20

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Asn
 1 5 10 15
 Arg Pro Ala Leu
 20

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Gly Ser Thr Ala Pro Pro Val His Asn Val Thr Ser Ala
 1 5 10

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1527 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...1524

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATG	ACA	CCG	GGC	ACC	CAG	TCT	CCT	TTC	TTC	CTG	CTG	CTG	CTC	CTC	ACA	48
Met	Thr	Pro	Gly	Thr	Gln	Ser	Pro	Phe	Phe	Leu	Leu	Leu	Leu	Leu	Thr	
1				5				10						15		
GTG	CTT	ACA	GCT	ACC	ACA	GCC	CCT	AAA	CCC	GCA	ACA	GTT	GTT	ACG	GGT	96
Val	Leu	Thr	Ala	Thr	Thr	Ala	Pro	Lys	Pro	Ala	Thr	Val	Val	Thr	Gly	
			20					25					30			
TCT	GGT	CAT	GCA	AGC	TCT	ACC	CCA	GGT	GGA	GAA	AAG	GAG	ACT	TCG	GCT	144
Ser	Gly	His	Ala	Ser	Ser	Thr	Pro	Gly	Gly	Glu	Lys	Glu	Thr	Ser	Ala	
			35				40					45				
ACC	CAG	AGA	AGT	TCA	GTG	CCC	AGC	TCT	ACT	GAG	AAG	AAT	GCT	GTG	AGT	192
Thr	Gln	Arg	Ser	Ser	Val	Pro	Ser	Ser	Thr	Glu	Lys	Asn	Ala	Val	Ser	
	50					55					60					
ATG	ACA	AGC	TTG	ATA	TCG	AAT	TCC	GGT	GTC	CGG	GGC	TCC	ACC	GCC	CCC	240
Met	Thr	Ser	Leu	Ile	Ser	Asn	Ser	Gly	Val	Arg	Gly	Ser	Thr	Ala	Pro	
65				70					75						80	
CCA	GCC	CAC	GGT	GTC	ACC	TCG	GCC	CCG	GAC	ACC	AGG	CCG	GCC	CCG	GGC	288
Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	
				85					90					95		
TCC	ACC	GCC	CCC	CCA	GCC	CAC	GGT	GTC	ACC	TCG	GCC	CCG	GAC	ACC	AGG	336
Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	
			100					105					110			
CCG	GCC	CCG	GGC	TCC	ACC	GCC	CCC	CCA	GCC	CAC	GGT	GTC	ACC	TCG	GCC	384
Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	
		115					120					125				
CCG	GAC	ACC	AGG	CCG	GCC	CCG	GGC	TCC	ACC	GCA	CCC	CCA	GCC	CAC	GGT	432
Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	
	130					135					140					
GTC	ACC	TCG	GCC	CCG	GAC	ACC	AGG	CGG	GCC	CCG	GGC	TCC	ACC	CCG	GCC	480
Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Arg	Ala	Pro	Gly	Ser	Thr	Pro	Ala	
145				150					155					160		
CCG	GGC	TCC	ACC	GCC	CCC	CCA	GCC	CAC	GGT	GTC	ACC	TCG	GCC	CCG	GAC	528
Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	
				165					170					175		
ACC	AGG	CCG	GCC	CCG	GGC	TCC	ACC	GCC	CCC	CCA	GCC	CAT	GGT	GTC	ACC	576
Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	
			180					185					190			
TCG	GCC	CCG	GAC	AAC	AGG	CCC	GCC	TTG	GGC	TCC	ACC	GCC	CCT	CCA	GTC	624
Ser	Ala	Pro	Asp	Asn	Arg	Pro	Ala	Leu	Gly	Ser	Thr	Ala	Pro	Pro	Val	
		195				200						205				
CAC	AAT	GTC	ACC	TCG	GCC	TCA	GGC	TCT	GCA	TCA	GGC	TCA	GCT	TCT	ACT	672
His	Asn	Val	Thr	Ser	Ala	Ser	Gly	Ser	Ala	Ser	Gly	Ser	Ala	Ser	Thr	
	210					215					220					
CTG	GTG	CAC	AAC	GGC	ACC	TCT	GCC	AGG	GCT	ACC	ACA	ACC	CCA	GCC	AGC	720
Leu	Val	His	Asn	Gly	Thr	Ser	Ala	Arg	Ala	Thr	Thr	Thr	Pro	Ala	Ser	

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225						230	235					240					
AAG Lys	AGC Ser	ACT Thr	CCA Pro	TTC Phe 245	TCA Ser	ATT Ile	CCC Pro	AGC Ser	CAC His 250	CAC His	TCT Ser	GAT Asp	ACT Thr	CCT Pro 255	ACC Thr	768	
ACC Thr	CTT Leu	GCC Ala	AGC Ser 260	CAT His	AGC Ser	ACC Thr	AAG Lys	ACT Thr 265	GAT Asp	GCC Ala	AGT Ser	AGC Ser	ACT Thr 270	CAC His	CAT His	816	
AGC Ser	ACG Thr	GTA Val 275	CCT Pro	CCT Pro	CTC Leu	ACC Thr	TCC Ser 280	TCC Ser	AAT Asn	CAC His	AGC Ser	ACT Thr 285	TCT Ser	CCC Pro	CAG Gln	864	
TTG Leu	TCT Ser 290	ACT Thr	GGG Gly	GTC Val	TCT Ser	TTC Phe 295	TTT Phe	TTC Phe	CTG Leu	TCT Ser	TTT Phe 300	CAC His	ATT Ile	TCA Ser	AAC Asn	912	
CTC Leu 305	CAG Gln	TTT Phe	CCT Pro	TCC Ser	TCT Ser 310	CTC Leu	GAA Glu	GAT Asp	CCC Pro	AGC Ser 315	ACC Thr	GAC Asp	TAC Tyr	TAC Tyr	CAA Gln 320	960	
GAG Glu	CTG Leu	CAG Gln	AGA Arg	GAC Asp 325	ATT Ile	TCT Ser	CAA Gln	ATG Met	TTT Phe 330	TTG Leu	CAG Gln	ATT Ile	TAT Tyr	AAA Lys 335	CAA Gln	1008	
GGG Gly	GGT Gly	TTT Phe	CTG Leu 340	GGC Gly	CTC Leu	TCC Ser	AAT Asn	ATT Ile 345	AAG Lys	TTC Phe	AGG Arg	CCA Pro	GGA Gly 350	TCT Ser	GTG Val	1056	
CTG Leu	GTA Val 355	CAA Gln	TTG Leu	ACT Thr	CTG Leu	GCC Ala	TTC Phe 360	CGA Arg	GAA Glu	GGT Gly	ACC Thr	ATC Ile 365	AAT Asn	GTC Val	CAC His	1104	
GAC Asp	GTG Val 370	GAG Glu	ACA Thr	CAG Gln	TTC Phe	AAT Asn 375	CAG Gln	TAT Tyr	AAA Lys	ACG Thr	GAA Glu 380	GCA Ala	GCC Ala	TCT Ser	CGA Arg	1152	
TAT Tyr 385	AAC Asn	CTG Leu	ACG Thr	ATC Ile	CCA Pro 390	GAC Asp	GTC Val	AGC Ser	GTG Val 395	AGT Ser	GAT Asp	GTG Val	CCA Pro	TTT Phe	CCT Pro 400	1200	
TTC Phe	TCT Ser	GCC Ala	CAG Gln	TCT Ser 405	GGG Gly	GCT Ala	GGG Gly	GTG Val 410	CCA Pro	GGC Gly	TGG Trp	GGC Gly	ATC Ile	GCG Ala 415	CTG Leu	1248	
CTC Leu	CTG Leu	CTG Leu	GTC Val 420	TGT Cys	GTT Val	CTG Leu	GTT Val	GCG Ala 425	CTG Leu	GCC Ala	ATT Ile	GTC Val	TAT Tyr 430	CTC Leu	ATT Ile	1296	
GCC Ala	TTG Leu	GCT Ala 435	GTC Val	TGT Cys	CAG Gln	TGC Cys	CGC Arg 440	CGA Arg	AAG Lys	AAC Asn	TAC Tyr	GGG Gly 445	CAG Gln	CTG Leu	GAC Asp	1344	
ATC Ile	TTT Phe 450	CCA Pro	GCC Ala	CGG Arg	GAT Asp	ACC Thr 455	TAC Tyr	CAT His	CCT Pro	ATG Met	AGC Ser 460	GAG Glu	TAC Tyr	CCC Pro	ACC Thr	1392	
TAC Tyr 465	CAC His	ACC Thr	CAT His	GGG Gly 470	CGC Arg	TAT Tyr	GTC Val	CCC Pro	CCT Pro	AGC Ser 475	AGT Ser	ACC Thr	GAT Asp	CGT Arg	AGC Ser 480	1440	
CCC	TAT	GAG	AAG	GTT	TCT	GCA	GGT	AAT	GGT	GGC	AGC	AGC	CTC	TCT	TAC	1488	

Pro Tyr Glu Lys Val Ser Ala Gly Asn Gly Gly Ser Ser Leu Ser Tyr
 485 490 495

ACA AAC CCA GCA GTG GCA GCC ACT TCT GCC AAC TTG TAG
 Thr Asn Pro Ala Val Ala Ala Thr Ser Ala Asn Leu
 500 505

1527

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 508 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Thr Pro Gly Thr Gln Ser Pro Phe Phe Leu Leu Leu Leu Leu Thr
 1 5 10 15
 Val Leu Thr Ala Thr Thr Ala Pro Lys Pro Ala Thr Val Val Thr Gly
 20 25 30
 Ser Gly His Ala Ser Ser Thr Pro Gly Gly Glu Lys Glu Thr Ser Ala
 35 40 45
 Thr Gln Arg Ser Ser Val Pro Ser Ser Thr Glu Lys Asn Ala Val Ser
 50 55 60
 Met Thr Ser Leu Ile Ser Asn Ser Gly Val Arg Gly Ser Thr Ala Pro
 65 70 75 80
 Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly
 85 90 95
 Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg
 100 105 110
 Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala
 115 120 125
 Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly
 130 135 140
 Val Thr Ser Ala Pro Asp Thr Arg Arg Ala Pro Gly Ser Thr Pro Ala
 145 150 155 160
 Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp
 165 170 175
 Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr
 180 185 190
 Ser Ala Pro Asp Asn Arg Pro Ala Leu Gly Ser Thr Ala Pro Pro Val
 195 200 205
 His Asn Val Thr Ser Ala Ser Gly Ser Ala Ser Gly Ser Ala Ser Thr
 210 215 220
 Leu Val His Asn Gly Thr Ser Ala Arg Ala Thr Thr Thr Pro Ala Ser
 225 230 235 240
 Lys Ser Thr Pro Phe Ser Ile Pro Ser His His Ser Asp Thr Pro Thr
 245 250 255
 Thr Leu Ala Ser His Ser Thr Lys Thr Asp Ala Ser Ser Thr His His
 260 265 270
 Ser Thr Val Pro Pro Leu Thr Ser Ser Asn His Ser Thr Ser Pro Gln
 275 280 285
 Leu Ser Thr Gly Val Ser Phe Phe Phe Leu Ser Phe His Ile Ser Asn
 290 295 300
 Leu Gln Phe Pro Ser Ser Leu Glu Asp Pro Ser Thr Asp Tyr Tyr Gln
 305 310 315 320
 Glu Leu Gln Arg Asp Ile Ser Gln Met Phe Leu Gln Ile Tyr Lys Gln
 325 330 335

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Gly	Gly	Phe	Leu	Gly	Leu	Ser	Asn	Ile	Lys	Phe	Arg	Pro	Gly	Ser	Val
			340					345					350		
Leu	Val	Gln	Leu	Thr	Leu	Ala	Phe	Arg	Glu	Gly	Thr	Ile	Asn	Val	His
		355					360					365			
Asp	Val	Glu	Thr	Gln	Phe	Asn	Gln	Tyr	Lys	Thr	Glu	Ala	Ala	Ser	Arg
		370				375					380				
Tyr	Asn	Leu	Thr	Ile	Pro	Asp	Val	Ser	Val	Ser	Asp	Val	Pro	Phe	Pro
385					390					395					400
Phe	Ser	Ala	Gln	Ser	Gly	Ala	Gly	Val	Pro	Gly	Trp	Gly	Ile	Ala	Leu
			405						410					415	
Leu	Leu	Leu	Val	Cys	Val	Leu	Val	Ala	Leu	Ala	Ile	Val	Tyr	Leu	Ile
			420					425					430		
Ala	Leu	Ala	Val	Cys	Gln	Cys	Arg	Arg	Lys	Asn	Tyr	Gly	Gln	Leu	Asp
		435					440					445			
Ile	Phe	Pro	Ala	Arg	Asp	Thr	Tyr	His	Pro	Met	Ser	Glu	Tyr	Pro	Thr
	450				455						460				
Tyr	His	Thr	His	Gly	Arg	Tyr	Val	Pro	Pro	Ser	Ser	Thr	Asp	Arg	Ser
465					470					475					480
Pro	Tyr	Glu	Lys	Val	Ser	Ala	Gly	Asn	Gly	Gly	Ser	Ser	Leu	Ser	Tyr
			485					490						495	
Thr	Asn	Pro	Ala	Val	Ala	Ala	Thr	Ser	Ala	Asn	Leu				
			500					505							

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Gly	Ser	Thr	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr
1				5					10					15		
Ser	Ala	Phe	Asp	Thr	Arg	Pro	Ala	Pro								
	20					25										